

GenCore version 5.1.4\_p5\_4578  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: March 15, 2003, 15:07:49 ; Search time 74.0238 Seconds  
(without alignments)  
1537.035 Million cell updates/sec

Title: US-08-978-217-16

Perfect score: 1985  
Sequence: 1 MATCEISNVFSNFTNMYMS.....YKFGKNSGCKKEEVEGSRN 371

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n model -DBV=1D  
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-DB=Issued\_Patents\_NA -QFMT=Isastag -SUFFIX=tni -MINMATCH=0.1 -LOOPL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-WARN\_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:\*  
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3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/prodata/1/ina/PCUTS\_COMB.seq:\*  
6: /cgn2\_6/prodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1712	86.2	1920	1	US-08-746-789A-1
2	586	29.5	5427	3	US-09-009-913-2
3	580	29.2	5510	3	US-09-009-913-3
4	580	29.2	5667	3	US-09-009-913-4
5	543	27.4	852	4	US-09-020-956-44
6	543	27.4	852	4	US-09-030-607-44
7	543	27.4	852	4	US-09-605-785-44
8	543	27.4	852	4	US-09-439-313-44
9	543	27.4	852	4	US-09-352-616A-44
10	543	27.4	852	4	US-09-232-149A-44
11	507	25.5	848	3	US-09-009-913-338
12	435.5	21.9	2280	3	US-09-009-913-8

13	435.5	21.9	2428	3	US-09-009-913-6	Sequence 6, Appl1
14	435.5	21.9	2498	3	US-09-009-913-10	Sequence 10, Appl1
15	238.5	12.0	2975	1	US-08-368-281-1	Sequence 1, Appl1
16	238.5	12.0	3240	1	US-08-368-281-3	Sequence 3, Appl1
17	234.5	11.8	1528	4	US-08-878-177-3	Sequence 3, Appl1
18	233.5	11.8	1905	4	US-09-055-113-2	Sequence 2, Appl1
19	225.5	11.4	1604	1	US-08-306-691B-43	Sequence 43, Appl1
20	225.5	11.4	1604	5	PCT-US93-06251-9	Sequence 9, Appl1
21	225	11.3	1447	4	US-08-878-177-1	Sequence 1, Appl1
22	225	11.3	2338	2	US-08-343-443B-3	Sequence 3, Appl1
23	220	11.1	2268	3	US-09-344-579-1	Sequence 1, Appl1
24	214	10.8	1752	4	US-09-360-779-1	Sequence 1, Appl1
25	214	10.8	1752	4	US-09-435-335-1	Sequence 1, Appl1
26	202.5	10.2	2266	2	US-09-213-767-1	Sequence 1, Appl1
27	180.5	9.1	2667	2	US-08-469-412A-1	Sequence 1, Appl1
28	180.5	9.1	2667	4	US-09-021-715-1	Sequence 1, Appl1
29	179	9.0	2410	2	US-08-780-835B-1	Sequence 1, Appl1
30	179	9.0	2410	4	US-09-303-268-1	Sequence 1, Appl1
31	179	9.0	2410	4	US-09-116-049-1	Sequence 1, Appl1
32	177	8.9	2064	3	US-08-875-944B-1	Sequence 1, Appl1
33	177	8.9	2064	4	US-09-116-049-3	Sequence 3, Appl1
34	145.5	7.3	1364	1	US-08-306-691B-50	Sequence 50, Appl1
35	145.5	7.3	1364	5	PCT-US93-06251-65	Sequence 65, Appl1
36	125	6.3	2544	2	US-08-469-412A-6	Sequence 6, Appl1
37	125	6.3	2544	4	US-09-021-715-6	Sequence 6, Appl1
38	104	5.2	2344	3	US-08-893-852A-2	Sequence 2, Appl1
39	100	5.0	3783	4	US-08-506-296B-20	Sequence 20, Appl1
40	99.5	5.0	3848	2	US-08-808-931-14	Sequence 14, Appl1
41	99.5	5.0	3848	3	US-08-808-323-14	Sequence 14, Appl1
42	99.5	5.0	3848	3	US-09-050-602A-14	Sequence 14, Appl1
43	99.5	5.0	3848	3	US-09-102-420B-14	Sequence 14, Appl1
44	99.5	5.0	3848	3	US-09-497-698-14	Sequence 14, Appl1
45	98	4.9	1476	4	US-09-434-288-12	Sequence 12, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-746-789A-1  
; Sequence 1, Application US/08746789A  
; Patent No. 5789200  
; GENERAL INFORMATION:  
; APPLICANT: Ismail Kola, Martin J. Tymins, Christine DeBouck  
; TITLE OF INVENTION: A No. 5789200el Human ETS Family Member, ELP3  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Smithkline Beecham Corporation  
; STREET: 709 Swedeland Road, P.O. Box 1539  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
; COMPUTER: IBM 486  
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
; SOFTWARE: MICROSOFT WORD  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/746,789A  
; FILING DATE: No. 5789200el 15, 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: William T. Han  
; REGISTRATION NUMBER: 34,344  
; REFERENCE/DOCKET NUMBER: ATG 50024  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610 270 5219  
; TELEFAX: 610 270 4026  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 1920  
 ; TYPE: Nucleic Acid  
 ; STRANDEDNESS: Single  
 ; TOPOLOGY: Linear  
 ; ANTI-SENSE: No  
 ; US-08-746-789A-1

Alignment Scores:  
 Pred. No.: 1.3e-173 Length: 1920  
 Score: 1712.00 Matches: 323  
 Percent Similarity: 92.74% Conservative: 22  
 Best Local Similarity: 86.83% Mismatches: 25  
 Query Match: 86.25% Indels: 2  
 Gaps: 2

US-08-978-217-16 (1-371) x US-08-746-789A-1 (1-1920)

QY 1 MetAlaAlaThrCysGluLysSerAsnValPheSerAsnTyrPheAsnAlaMetTyrSer 20  
 Db 115 ATGGCTGCAACCTGAGATTGCAACATTTTACCACTTCTCAGTCCGATGACAGC 174  
 QY 21 SerGluAProThrLeuAlaProAlaProPro---ThrThPheGlyThrGluAspLeu 39  
 Db 175 TCGGAGACTCCACCTTGCCCTGCTGCTCCCTGCTGCCACCTTGGGGCGGATGACTTG 234  
 QY 40 ValLeuThrLeuAsnAsnGlnGlnMetThrLeuGluGlyProGluLysAlaSerTyrThr 59  
 Db 235 GTACTGACCTGAGCAACCCCGAGATGATCGAGGGGACAGAGAAAGGCTGCTGTTG 294  
 QY 60 SerGluAProGlnPheTyrSerTyrThrGlnValLeuGluTyrPheSerGlnVal 79  
 Db 295 GGGGAACAGCCCACTGCTGTCGAAAGCAGGTTTGGATGATGATCAACCAAGTG 354  
 QY 80 GluLysAsnLysTyrAspAlaSerSerLysPheSerArgCysAsnMetAspGlyAla 99  
 Db 355 GAGAAGAACAGTACGAGCAGCAGCCCATGACTTCTCAGATGATGATGAGGGCC 414  
 QY 100 ThrLeuCysSerCysAlaLeuGluGluLeuArgLysValPheGlyProLeuGlyAspGln 119  
 Db 415 ACCCTCTCAATTGTCCTTGAGAGAGCTGCTGCTGTTGGGCGCTGCGGGACCAA 474  
 QY 120 LeuHisAlaGlnLeuArgAspLeuThrSerAsnSerSerAspGluLeuSerTyrPhe 139  
 Db 475 CTCCATGCCAGCTCGAGACTCTCAGCTTCTGATGATGATGATGATGATGAT 534  
 QY 140 GluLeuLeuGluLysAspGlyMetSerPheGlnGlnLysLeuGlyAspLeuGlyProPhe 159  
 Db 535 GAGCTGCTGGAAGATGATGATGCTTCCAGAGGCGCTTA--GACCCAGGCGCTTT 591  
 QY 160 AspGlnGlySerProPheAlaGlnGlnLeuLeuAspAspGlyArgGlnAlaSerProTyr 179  
 Db 592 GACCAAGGCAAGCCCTTTCAGAGAGCTGCTGAGAGAGCTGACAGAGCCAGCCCTTTC 651  
 QY 180 TyrCysSerThrTyrGlyProGlyAlaProSerProGlySerSerAspValSerThrAla 199  
 Db 652 CACCCGGCAGCTGAGCGCAGAGAGCCCTCCCTCGAGAGCTGAGAGCTCCACCGCA 711  
 QY 200 ArgThrAlaThrProGlnSerSerThrAlaSerAspSerGlyLysSerAspValAspLeu 219  
 Db 712 GGGACTGCTGCTTCTCGAGAGCTCCCACTCTCAGACTCGGAGGAGAGAGCTGAGAGCTG 771  
 QY 220 AspLeuThrGlnLysSerLysValPheProArgAspAspPheThrAspTyrLysLysGlyAla 239  
 Db 772 GATCCCACTGATGAGCAAGCTTTCCTCCAGCATGCTTTTCGATCAGCAAGAGGGGAT 831  
 QY 240 ProLysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGlyLysTyrPheAsp 259  
 Db 832 CCGAAGCAACGGGAAGCGGAAGAGAGCGCGCCCGAAGAGCTAGCAAGAGAGTACGGAGC 891  
 QY 260 CysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTyrGluPheIle 279  
 Db 892 TGCTCTGAGGGGCAAG 951

QY 280 ArgAspIleLeuIleHisProGlnLeuAsnGluGlyLeuMetLysTyrGluAsnArgHis 299  
 Db 952 CGGAGCATCTTCATCCACCGGAGCTCAACGAGGGCTTCATGAGTGGAGAAATCGGCAT 1011  
 QY 300 GluGlyValPheLysPheLeuArgSerGlnAlaValAlaGlnLeuTyrPheGlnLysLys 319  
 Db 1012 GAAGCGCTTCAAGTCTCGCGCTCCGAGGCTGTGCGCCCAACTATAGGGGCAAGAA 1071  
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 Db 1132 GAGATCTCGAAGCGGTGAGTGGCGGCGAGCTCGTACAAAGTTGGCAAAACTCAAGC 1191  
 QY 360 GlyTyrPheGluGluGluValGlyGlyLysSerArgAsn 371  
 Db 1192 GCGTGAAGAGAGAGAGAGTTCACAGATCGGAAC 1227  
 RESULT 2  
 US-09-009-913-2  
 ; Sequence 2, Application US/0909913  
 ; Patent No. 6087485  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Axy's Pharmaceuticals, Inc.  
 ; TITLE OF INVENTION: Asthma Related Genes  
 ; NUMBER OF SEQUENCES: 339  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Bozicevic & Reed, LLP  
 ; STREET: 285 Hamilton Ave, Suite 200  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94301  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/009, 913  
 ; FILING DATE: 21-JAN-1998  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sherwood, Pamela J  
 ; REGISTRATION NUMBER: 36,677  
 ; REFERENCE/DOCKET NUMBER: SEQ-4P  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650-327-3231  
 ; TELEFAX: 650-327-3231  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5427 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; US-09-009-913-2  
 Alignment Scores:  
 Pred. No.: 2.58e-52 Length: 5427  
 Score: 586.00 Matches: 141  
 Percent Similarity: 50.26% Conservative: 51  
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 Gaps: 11

US-08-978-217-16 (1-371) x US-09-009-913-2 (1-5427)



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Oy 135 LeuSerTrpIleIleGluLeuLeuGluLysAspGluMetSerPheGlnGluSerLeuGly 154
Db 593 -----CTGTTCCAGTCCACACACAACT 613
Oy 155 AspLeuGlyProPheAspGlnGlySerProPheAlaGlnGluLeuLeuAspArgLysArg 174
Db 614 GTCAATTGTCAGAGCTGAACAAACTGACCT-----TCCATCTCATGACACCTGGAAA 664
Oy 175 GlnAlaSerProGlyTrpCysSerThrTyrGlyProGlyValaProSerProGlySerSer 194
Db 665 GACGAGAACTTTATATATGACACCACTATGGT----- 697
Oy 195 AspValSerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAspSerGlyGly 214
Db 698 -----ACGACA----- 703
Oy 215 SerAspValaAspLeuAspLeuThrGlnSerLysValaPheProArgAspAspPhe----- 232
Db 704 -----GNAGATTTGTTGGACAGCAAAACTTTTCGCCGGGCTCAGATCTCCATG 751
Oy 233 -----ThrAspTrpLysGlyGluProLysHisGlyLysAspArgLysArgLysArg 249
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Oy 250 ProArgLysLeuSerLysGluTrpAspCysLeuGlnGlyLysLysSerLysHisAla 269
Db 812 CCTGCCAAGTCCACCAACAAA-----AAGCACAAAC 841
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Oy 290 GluGlyLeuMetLysTrpGluAsnArgHisGluGlyValaPheLysPheLeuArgSerGlu 309
Db 902 CCAGATTAAATAAATATGGAAAGACCCATCTGAGGGCGCTCTTCACGTTCTTGAATACTAGAG 961
Oy 310 AlaValaAlaGlnLeuTrpGlyGlnLysLysLysAsnSerAsnMetThrTyrGluLysLeu 329
Db 962 GCAGTGGCTCATCTATGGGGTAAAAAAAAGAACACACGCGCATGTGACATGAAAAAGCTTC 1021
Oy 330 SerArgAlaMetArgTyrTyrTyrLysArgGluIleGluGlnArgValaAspArgArgArg 349
Db 1022 AGCCAGGCTTAAGAATATTACTACAAAGAAGAAATACTGAGCGCTGGATGAGACGAAGA 1081
Oy 350 LeuValTyrLysPheGlyLysAsnSerSerGlyTrpLysGluGluGlu 365
Db 1082 CTGGTATATAAATTTGGGAGAAATGCCCGAGATGAGAGAAAAATGAA 1129

RESULT 4
US-09-009-913-4
; Sequence 4, Application US/09009913
; Patent No. 6087485
; GENERAL INFORMATION:
; APPLICANT: Axxis Pharmaceuticals, Inc.
; TITLE OF INVENTION: Asthma Related Genes
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/009,913
: FILING DATE: 21-JAN-1998
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Sherwood, Pamela J
: REGISTRATION NUMBER: 36,677
: REFERENCE/DOCKET NUMBER: SEQ-4P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-327-3231
: TELEFAX: 650-327-3231
: TELEX:
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5667 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-09-009-913-4

Alignment Scores:
Pred. No.: 1,21e-51 Length: 5667
Score: 580.00 Matches: 129
Percent Similarity: 54.43% Conservative: 43
Best Local Similarity: 40.82% Mismatches: 78
Query Match: 29.22% Indels: 66
DBs: 3 Gaps: 7

US-08-978-217-16 (1-371) x US-09-009-913-4 (1-5667)
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QY 78 GlnValGluIlyValLeuIlyTyrAspAlaSerSerIleAspPheSerIleArgCysAsnMetAsp 97
Db 573 CTCCTGGACACCAACCAAGCTGGATGCCAATTGTATCCCTTCCAGAGTTCGACATCCAC 6322
QY 98 GlyAlaThrLeuCysSerCysAlaLeuGluGluLeuArgLeuValPheGlyProLeuGly 117
Db 633 GCGGAGCACCTTCGAGAGTACAGTTCACCGGGCGGCGAGGAGCGCGGG 6322
QY 118 AspGlnLeuHisAlaGlnLeuArgAspLeuThrSerAsn-----SerSerAspGlu 134
Db 693 CAGCTCCCTCTACACCACTTCGACACATCTGAAGTGAACGCGCAGTGCACATAGTAC-- 749
QY 135 LeuSerTrpIleIleGluLeuLeuGluIlyAspGlyMetSerPheGlnGluSerLeuGly 154
Db 750 -----CTGTTCCAGTCCACACACCAAT 770
QY 155 AspleuGlyProPheAspGlnGlySerProPheAlaGlnGluLeuAspAspGlyArg 174
Db 771 GTCATTGTCAAGACTGAACCAACTGAGCCT-----TTCATCATGAACACCTGGAAA 821
QY 175 GlnAlaSerProTyrTyrCysSerThrTyrGlyProGlyAlaProSerProGlySerSer 194
Db 822 GACGGAACCTTTATATGACACCAACTATGT----- 854
QY 195 AspValSerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAspSerglyGly 214
Db 855 -----ACGACA----- 860
QY 215 SerAspValAspLeuAspLeuThrGlnSerIlyValAlaPheProArgAspAspPhe----- 232
Db 861 -----GTAGATTGCTTGGAACAGCAAACTTTCTGCGGGCTCAGATCTCCATG 908
QY 233 -----ThrAspTyrIlyLeuGlyGluProIlyHisGlyIlyAspArgIlyArg 249
Db 909 ACACACCAAGCACCTTCTGTTGCGACAGTCAAGTCACTATATGAAAAAGAGCAAGACCCC 968

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QY 250 ProArgIysLeuSerIysGluTyrTrpAspCysLeuGluGlyIysSerIysHisAla 269  
 DB 969 CCGCCAAAGTGCACACACAAA-----AAACCAAC 998  
 QY 270 ProArgIyThrHisLeuTrpGluPheIleArgAspIleLeuIleHisProGluLeuAsn 289  
 DB 999 CCGAGAGGAGCTACCTATGGAATTCATCCGACATCCCTTGAACCCAGACAAAGAAC 1058  
 QY 290 GluGlyLeuMetCysTrpGluAsnArgHisGluGlyValPheIysPheLeuArgSerGlu 309  
 DB 1059 CCGAGATTATATAAATGGAGAGACCGATCTGAGGCGCTCTTCAAGTCTTGAATCAAG 1118  
 QY 310 AlaValAlaGlnLeuTrpGlyGlnIysIysIysAsnSerAsnMetTrpGlyGlyLeu 329  
 DB 1119 GCAGTGCCTCAGCTATGCGGTAAAGAAAGAACACAGCAGCATGACCTATGAAAGCTC 1178  
 QY 330 SerArgAlaMetArgIyTrpTrpIysArgGluIleLeuGluValAspGlyArg 349  
 DB 1179 AGCGGACCTATGAGATTTACTACAAAAGAAATGCTGGCGCTCTGATGAGCAAGA 1238  
 QY 350 LeuValIysIysPheGlyIysAsnSerSerGlyTrpIysGluGlu 365  
 DB 1239 CTGGTATATATAATTGGGAAGATGCCGAGATGAGAGAAATGAA 1286  
 RESULT 5  
 US-09-020-956-44/C  
 ; Sequence 44, Application US/09020956  
 ; Patent No. 6261562  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillin, Davin C.  
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO  
 ; NUMBER OF SEQUENCES: 178  
 ; CORRESPONDENCE ADDRESS: 178  
 ; ADDRESSEE: SEED and BERRY LLP  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98104  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/020, 956  
 ; FILING DATE: 09-FEB-1998  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Maki, David J.  
 ; REGISTRATION NUMBER: 31,392  
 ; REFERENCE/DOCKET NUMBER: 210121.42762  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 44:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 852 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Homo sapiens  
 ; US-09-020-956-44  
 Alignment Scores:  
 Pred. No.: 5.98e-49 Length: 852  
 Score: 543.00 Matches: 124  
 Percent Similarity: 54.28% Conservative: 41  
 Best Local Similarity: 40.79% Mismatches: 73

Query Match: 27.36% Indels: 66  
 DB: 4 Gaps: 7  
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 QY 70 GlnValLeuGluTrpIleSerTrpGlnValGlnIysAsnIysTrpAspAlaSerIle 89  
 DB 850 CAGGTGGGAGGAGGCTCCACATCTCCAGACCAACCAAGTGGATGGCAATTGATC 791  
 QY 90 AspPheSerArgCysAsnMetAspGlyAlaThrLeuCysSerCysAlaLeuGluLeu 109  
 DB 790 CTTTCCANAGTTCCACATCAACGGCGAGACACTTTGCGCATGACTTTGCGAGCTC 721  
 QY 110 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSer 129  
 DB 730 ACCCGGGCGGAGGAGCGGGGCGCANCTCCTCAACGAACTTGCAGCATCGAAGTGG 671  
 QY 130 Asn-----SerSerArgIleLeuSerTrpIleIleGluLeuGluIysAspGly 146  
 DB 670 AACGGCCAGTCAGTGTGAC----- 650  
 QY 147 MetSerPheGlnGluSerLeuGlyAspLeuGlyProPheAspGlnGlySerProPheAla 166  
 DB 649 ---CTGTTCCAGTCCACACAAATGTCATTGTCAAGACTGAACAACTGAGCT--- 559  
 QY 167 GlnGluLeuLeuAspArgIysArgGlnAlaSerProTrpTrpCysSerThrTrpGlyPro 186  
 DB 598 ---TCCATCATGAACACCTGGAAGACNAGACTATTATATGACCACTATGCT--- 545  
 QY 187 GlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrProGlnSer 206  
 DB 544 -----AGCACA----- 539  
 QY 207 SerHisAlaSerAspSerGlyIysSerAspValAspLeuAspLeuThrGluSerIysVal 226  
 DB 538 -----GTAAATTTGTTGGACAGCAAACT 515  
 QY 227 PheProArgAspAspPhe-----ThrAspTrpIysGlyGlyProIys 241  
 DB 514 TTCGCCGGGCTCAGATCTCCATGACAAACCAACGACTCCTCTGTGAGAGTCACT 455  
 QY 242 HisGlyIysArgIysArgIysArgProArgIysLeuSerIysGluTrpAspCysLeu 261  
 DB 454 GATATGAAAAAGAGCAAGCCGCCCTGCCAAGTGCACACCAAA----- 410  
 QY 262 GluGlyIysSerIysHisAlaProArgGlyThrHisLeuTrpGluPheIleArgAsp 281  
 DB 409 -----AAGCAAAACCGAGAGGAGCTCACTTATGGGAATTCATCCGAC 365  
 QY 282 IleLeuIleHisProGluLeuAsnGluGlyLeuMetCysTrpGluAsnArgHisGluGly 301  
 DB 364 ATCTCTTGAACCCAGACAAAGAACCCAGGATTATATAAAGGAAAGCCATCTGAGGCG 305  
 QY 302 ValPheIysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnIysIysAsn 321  
 DB 304 GCTTCAGGTTCTTGAATATCAGAGGAGGCTCAGCTATGAGGTAAAGAAAGCAAC 245  
 QY 322 SerAsnMetThrTrpGlyIysLeuSerArgAlaMetArgTrpTrpTrpIysAsnGluIle 341  
 DB 244 AGCAGCATGACCTATGAAAGCTCAGCGGCTATGAGATTAATTAACAAAGAAATTT 185  
 QY 342 LeuGluArgValAspGlyArgLeuValTrpIysPheGlyIysAsnSerSerGlyTrp 361  
 DB 184 CTGAGGCTGTGATGACCAAGACTGTATATATAATTGGGAAGATGCCAGAGATGG 125  
 QY 362 LysGluGluGlu 365  
 DB 124 AGAGAAAAATGAA 113  
 RESULT 6  
 US-09-030-607-44/C  
 ; Sequence 44, Application US/09030607  
 ; Patent No. 6262245

```

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Circle, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030.607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mark, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 852 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-030-607-44

Alignment Scores:
Pred. No.: 5,98e-49 Length: 852
Score: 543.00 Matches: 124
Percent Similarity: 54.28% Conservative: 41
Best Local Similarity: 40.79% Mismatches: 73
Query Match: 27.36% Indels: 66
DB: 4 Gaps: 7

US-08-978-217-16 (1-371) x US-09-030-607-44 (1-852)
Qy 70 GlnValLeuGluTrpIleSerTyrglnValGluLysAsnLysTyAspAlaSerSerIle 89
Db 850 CAGGTGGGATGGCTCATCATCCCTCGACACCAACCACTGATGCAATGTATC 791
Qy 90 AspPheSerArgCysAsnMetAspGlyAlaThrLeuCysSerCysAlaLeuGluGluLeu 109
Db 790 CTTTCCACGAGTTCATCATCAACGCGGACGACCTTTGACGATGATGTTGACGAGATTTC 731
Qy 110 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSer 129
Db 730 ACCCGGGGCGGACGAGCGGGGACNCTCTCTACAGCACTTGACGATGAGATCGAAGTGG 671
Qy 130 Aen-----SerSerAspGluLeuSerTrpIleIleGluLeuLeuGluLysAspGly 146
Db 670 AACGGCCAGTGCATGATGAC----- 650
Qy 147 MetSerPheGlnGluSerLeuGlyAspLeuGlyProPheAspGlnGlySerProPheAla 166
Db 649 ---CTGTTCAGTCCACACACATGTCATTTGCAAGACTGACCAAACTGAGCCT----- 599
Qy 167 GlnGluLeuLeuAspGlyArgGlnAlaSerProTyTyTyCysSerThrTyGlyPro 186
Db 598 ---TCCATCATGACCACTGMAAGACNAGAACTATTATATGACCAACCAATATGTGT--- 545

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Qy 187 GlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrProGlnSer 206
Db 544 -----AGCACA----- 539
Qy 207 SerHisAlaSerAspSerGlyGlySerAspValAspLeuAspLeuThrGluSerLysVal 226
Db 538 -----GTAGATTGTTGGACAGCAAACT 515
Qy 227 PheProArgAspAspPhe-----ThrAspTyrlLysLysGlyLysProLys 241
Db 514 TTCTGCGGCGCTCAGATCTCCATGACCAACCAAGTACCTCTGTTGACAGATCACT 455
Qy 242 HisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGlyTyTrpAspCysLeu 261
Db 454 GATATGAAAAAGAGCAAGACCCCTCCCAAGTGCACACCAAA----- 410
Qy 262 GluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIleArgAsp 281
Db 409 -----AGCACAAACCCGAGAGGAGCTCATATGGGAATTCATCCGCGAC 365
Qy 282 IleLeuHisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHisGluGly 301
Db 364 ATCTCTTGAACCCAGACACCAAGACCAAGATTAATAAATGGAAAGACCATCTGAGGGC 305
Qy 302 ValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLysLysAsn 321
Db 304 GTCTTCAGGTTCTTGAATCAGAGGCAAGTGGCTCAGCTATGGGTAAAGAAACCAAC 245
Qy 322 SerAsnMetThrTyrgluLysLeuSerArgHisMetArgTyTyTyTyLysArgGluHis 341
Db 244 AGCAGCATGACCTATGAAAGCTCAGCCGAGCTATGAGATTAATCTACAAAGAAATTT 185
Qy 342 LeuGluArgValAspGlyArgArgLeuValTyrlLysPheGlyLysAsnSerSerTyTrp 361
Db 184 CTGAGCCTGTGATGACGAGCAAGACTGTATATAATTGGGAAGAAATGCCCGAGATGG 125
Qy 362 LysGluGluGlu 365
Db 124 AGAGAAATGAA 113

RESULT 7
US-09-605-785-44/C
Sequence 44, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605.785
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 44
LENGTH: 852
TYPE: DNA
ORGANISM: Homo sapien

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FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(852)
; OTHER INFORMATION: n = A,T,C or G
US-09-605-785-44

Alignment Scores:
Pred. No.: 5,98e-49 Length: 852
Score: 543.00 Matches: 124
Percent Similarity: 54.28% Conservative: 41
Best Local Similarity: 40.79% Mismatches: 73
Query Match: 27.36% Indels: 66
DB: Gaps: 7

US-08-978-217-16 (1-371) x US-09-605-785-44 (1-852)
QY 70 GlnValLeuGluTrpLieserTyrgInValGluLeuAsnTyrrAspAlaSerSerIle 89
DB 850 CAGGTGTGGAGTGGCTCCATCCCTCTGGACACCAACGATGATGCCAATTGTATC 791
QY 90 AspPheSerArgCysAsnMetAepGlyAlaThrLeuCysSerCysAlaLeuGluLeu 109
DB 790 CCTTCCANAGTTCCACATCAACGCGAGACCTTTGCACATGAGTTGCAGAGATTC 731
QY 110 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSer 129
DB 730 ACCCGGCGGAGGAGCGCGGGCANCCTCTACAGCAACTTGACAGCATCTGAATGG 671
QY 130 Asn-----SerSerArgGluLeuSerTrpIleIleGluLeuLeuGluLysAspGly 146
DB 670 AACGGCCAGTGCAGTATGAC----- 650
QY 147 MetSerPheGlnGluSerLeuGlyAspLeuGlyProPheAspGlnGlySerProPheAla 166
DB 649 ----CTGTTCCAGTCCACACACATGTCATTGTCAAGACTGAACAACTGAGCT- 599
QY 167 GlnGluLeuLeuAspArgGlyArgGlnAlaSerProTyrrCysSerThrTyrglyPro 186
DB 598 ---TCCATCATGAACACCTCGAAGACNAGAACTATTATATGACACCACTATGCT- 545
QY 187 GlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaProGlnSer 206
DB 544 -----AGCACA----- 539
QY 207 SerHisAlaSerAspSerGlyGlySerAspValAspLeuAspLeuThrGlnSerIleVal 226
DB 538 -----GTAGATTGTGGACAGCAAACT 515
QY 227 PheProArgAspAspPhe-----ThrAspTyrrLysLysGlyGluProLys 241
DB 514 TTCTGCCGGCTCGATCTCCATGACAAACCACTGACCTTCTGTTCAGAGTCACT 455
QY 242 HisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGluTyrrTrpAspCysLeu 261
DB 454 GATATGAAAAAGGAGCAAGACCCCTGCCAAGTCCACACCAAA----- 410
QY 262 GlnGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIleArgAsp 281
DB 409 -----AAGCACAAACCCGAGAGGACTCACTTATGGAATTATCATCCGGAC 365
QY 282 IleLeuIleHisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHisGluGly 301
DB 364 ATCTCTTGAACCCAGACACAGAACCCAGATTAATAATGGAAAGCCATCTGAGGCG 305
QY 302 ValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLysLysAsn 321
DB 304 GTCTTCAGTTCCTTGAATACAGAGGAGTGGCTCAGCTATGGGTAAGAAAGAACAC 245
QY 322 SerAsnMetThrTyrrGluLysLeuSerArgAlaMetArgTyrrTyrrLysArgGluIle 341
DB 244 AGCAGCATGACCTATGAAAAAGCTTACCGGAGCTATGAGATTAATTAACAAAGGAATT 185
QY 342 LeuGluArgValAspGlyArgArgLeuValTyrrLysPheGlyLysAsnSerSerGlyTrp 361

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DB 184 CTGAGCGTGTGATGAGACCAAGCTGTATATTAATTGGAGAAATGCCGAGAGATGG 125
QY 362 LysGluGluGlu 365
DB 124 AGAGAAATGAA 113

RESULT 8
US-09-439-313-44/C
; Sequence 44, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kaloje, Gary
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 852
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(852)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-44

Alignment Scores:
Pred. No.: 5,98e-49 Length: 852
Score: 543.00 Matches: 124
Percent Similarity: 54.28% Conservative: 41
Best Local Similarity: 40.79% Mismatches: 73
Query Match: 27.36% Indels: 66
DB: Gaps: 7

US-08-978-217-16 (1-371) x US-09-439-313-44 (1-852)
QY 70 GlnValLeuGluTrpLieserTyrgInValGluLeuAsnTyrrAspAlaSerSerIle 89
DB 850 CAGGTGTGGAGTGGCTCCATCCCTCTGGACACCAACGATGATGCCAATTGTATC 791
QY 90 AspPheSerArgCysAsnMetAepGlyAlaThrLeuCysSerCysAlaLeuGluLeu 109
DB 790 CCTTCCANAGTTCCACATCAACGCGAGACCTTTGCACATGAGTTGCAGAGATTC 731
QY 110 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSer 129
DB 730 ACCCGGCGGAGGAGCGCGGGCANCCTCTACAGCAACTTGACAGCATCTGAATGG 671
QY 130 Asn-----SerSerArgGluLeuSerTrpIleIleGluLeuLeuGluLysAspGly 146
DB 670 AACGGCCAGTGCAGTATGAC----- 650
QY 147 MetSerPheGlnGluSerLeuGlyAspLeuGlyProPheAspGlnGlySerProPheAla 166
DB 649 ----CTGTTCCAGTCCACACACATGTCATTGTCAAGACTGAACAACTGAGCT- 599
QY 167 GlnGluLeuLeuAspArgGlyArgGlnAlaSerProTyrrCysSerThrTyrglyPro 186
DB 598 ---TCCATCATGAACACCTCGAAGACNAGAACTATTATATGACACCACTATGCT- 545

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QY 187 GlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrProGlnSer 206  
 DB 544 -----AGCACA----- 539  
 QY 207 SerHisAlaSerAspSerGlyGlySerAspValAspLeuAspLeuThrGlnSerIleVal 226  
 DB 538 -----GTGATTTTGTGGACGCAAAACT 515  
 QY 227 PheProArgAspAspPhe-----ThrAspTyrIleGlyGlyGluProIleVal 241  
 DB 514 TTCTGCGGGGCTCAGATCTCCATGACACACCACTCTCTGTTGACAGTCACCT 455  
 QY 242 HisGlyLysArgLysArgGlyLysArgLysLeuSerLysGlnTyrTrpAspCysLeu 261  
 DB 454 GATATGAAAAAGAGACAAACCCCTGCGCAAGTGCACACAAA----- 410  
 QY 262 GlnGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGlnPheIleArgAsp 281  
 DB 409 -----AAGCACAACCCGAGAGGAGCTCTTATGGAAATTCAATCCCGCAC 365  
 QY 282 IleLeuIleHisProGlnLeuAsnGlnGlyLeuMetLysTrpGlnAsnArgHisGlnGly 301  
 DB 364 ATCTCTTGAACCCGACAGAACCCAGATTAATAAATGGAAAGACCGATCTGAGGCG 305  
 QY 302 ValPheLysPheLeuArgSerGlnValAlaAlaGlnLeuTrpGlnLysLysIleAsn 321  
 DB 304 GTCTTCAGGTTCTTGAATCAGAGGAGTGCTCAGCTATGGGGTAAAAAGAAACAAAC 245  
 QY 322 SerAsnMetThrTyrGlnLysLeuSerArgAlaMetArgTyrTyrTyrLysArgGlnIle 341  
 DB 244 AGCACAATGACCTATGAAAAAGCTCAGCCGATATGAGATATTAATCAAAAAAGAGAAAT 185  
 QY 342 LeuGlnArgValAspGlyLysArgLysLeuValTyrLysPheGlnLysAsnSerSerGlyTyr 361  
 DB 184 CTGGAGCGTGTGATGAGCAAGAGCTGTATTAATTTGGAAAGATCCCGAGATGG 125  
 QY 362 LysGlnGlnGln 365  
 DB 124 AGAGAAATGAA 113

Query Match: 27.36% Indels: 66  
 DB: 4 Gaps: 7  
 US-08-978-217-16 (1-371) x US-09-352-616A-44 (1-852)  
 QY 70 GlnValLeuGlnTyrPheIleSerTyrGlnValGlnLysAsnLysTyrAspAlaSerSerIle 89  
 DB 850 CAGGTGTGGAGTGTGCTCATCTCCTCCTGACCAACCAACCGCTGAGTGAATTTGATTC 791  
 QY 90 AspPheSerArgCysAsnMetAspGlyAlaThrLeuCysSerCysAlaLeuGlnGluLeu 109  
 DB 790 CCTTTCANAGAGTTGACATATCAACGCGAGACCTTTGACACATGAGTTTCAGAGATTC 731  
 QY 110 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSer 129  
 DB 720 ACCGCGGCGAGGAGCGCGGCGCANCTCCTTAACAGCACTTGACAGCATCTGAAGTGG 671  
 QY 130 Asn-----SerSerAspGlnLeuSerTrpIleIleGlnLeuLeuGlnLysAspGly 146  
 DB 670 AACGCGCAGTCAGTATGAC----- 650  
 QY 147 MetSerPheGlnGlnLysSerLeuGlnLysAspLeuGlyProPheAspGlnGlySerProPheAla 166  
 DB 649 ---CTGTTCCAGTCCACACACAAATGTCTATTGTCAAGACTGAACAAACTGAGCCT----- 599  
 QY 167 GlnGlnLeuLeuAspAspGlyLysGlnAlaSerProTyrTyrCysSerThrTyrGlyPro 186  
 DB 598 ---TCCATCATGACACACTGGAAAGACAAAGAACTATTATATGACACCAACTATGGT--- 545  
 QY 187 GlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrProGlnSer 206  
 DB 544 -----AGCACA----- 539  
 QY 207 SerHisAlaSerAspSerGlyLysSerAspValAspLeuAspLeuThrGlnSerIleVal 226  
 DB 538 -----GTGATTTTGTGGACGCAAAACT 515  
 QY 227 PheProArgAspAspPhe-----ThrAspTyrLysLysGlyGluProIleVal 241  
 DB 514 TTCTGCGGGGCTCAGATCTCCATGACACACAGTCACTTCTGTTGACAGTCACCT 455  
 QY 242 HisGlyLysArgLysArgGlyLysArgLysLeuSerLysGlnTyrTrpAspCysLeu 261  
 DB 454 GATATGAAAAAGAGACAAACCCCTGCGCAAGTGCACACAAA----- 410  
 QY 262 GlnGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGlnPheIleArgAsp 281  
 DB 409 -----AAGCACAACCCGAGAGGAGCTCTTATGGAAATTCAATCCCGCAC 365  
 QY 282 IleLeuIleHisProGlnLeuAsnGlnGlyLeuMetLysTrpGlnAsnArgHisGlnGly 301  
 DB 364 ATCTCTTGAACCCGACAGAACCCAGATTAATAAATGGAAAGACCGATCTGAGGCG 305  
 QY 302 ValPheLysPheLeuArgSerGlnValAlaAlaGlnLeuTrpGlnLysLysIleAsn 321  
 DB 304 GTCTTCAGGTTCTTGAATCAGAGGAGTGCTCAGCTATGGGGTAAAAAGAAACAAAC 245  
 QY 322 SerAsnMetThrTyrGlnLysLeuSerArgAlaMetArgTyrTyrTyrLysArgGlnIle 341  
 DB 244 AGCACAATGACCTATGAAAAAGCTCAGCCGATATGAGATATTAATCAAAAAAGAGAAAT 185  
 QY 342 LeuGlnArgValAspGlyLysArgLysLeuValTyrLysPheGlnLysAsnSerSerGlyTyr 361  
 DB 184 CTGGAGCGTGTGATGAGCAAGAGCTGTATTAATTTGGAAAGATCCCGAGATGG 125  
 QY 362 LysGlnGlnGln 365  
 DB 124 AGAGAAATGAA 113

Alignment Scores: 5,98e-49 Length: 852  
 Score: 543.00 Matches: 124  
 Percent Similarity: 54.28% Conservative: 41  
 Best Local Similarity: 40.79% Mismatches: 73

RESULT 10  
 US-08-232-149A-44/C  
 ; Sequence 44, Application US/09232149A  
 ; Patent No. 6465611



GENERAL INFORMATION:  
 APPLICANT: Xu, Jiangchun  
 APPLICANT: Dillon, Davin C.  
 APPLICANT: Mitcham, Jennifer Lynn  
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE  
 TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE  
 FILE REFERENCE: 210121.427C6  
 CURRENT APPLICATION NUMBER: US/09/232.149A  
 CURRENT FILING DATE: 1999-01-15  
 NUMBER OF SEQ ID NOS: 338  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 44  
 LENGTH: 852  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)...(852)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-232-149A-44

Alignment Scores:  
 Pred. No.: 5.98e-49 Length: 852  
 Score: 543.00 Matches: 124  
 Percent Similarity: 54.28% Conservative: 41  
 Best Local Similarity: 40.79% Mismatches: 73  
 Query Match: 27.36% Indels: 66  
 Gaps: 7  
 DB: 4

US-08-978-217-16 (1-371) x US-09-232-149A-44 (1-852)

QY 70 GlnValLeuGluTrpIleSerTyGlnValGluLysAsnLysTyRAspAlaSerSerIle 89  
 DB 850 CAGGTGGGAGTGGTCCATCATCCTCTGAGACCAACGCGATGCAATGATATC 791  
 QY 90 AspPheSerArgCyAsnMetAspGlyAlaThrLeuCySerCyAlaLeuGluGlu 109  
 DB 790 CCTTCCAGATGTCATCATCAACGCGACGACCTTGACAGATGTTGACAGAGTTC 731  
 QY 110 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuAspLeuThrSer 129  
 DB 730 ACCCGGCGGAGGAGCGCGCGGCACTCTTACAGCAACTTGACAGCATCTAAGTGG 671  
 QY 130 Asn-----SerSerAspGluLeuSerTrpIleIleGluLeuGluLysAspGly 146  
 DB 670 AACGGCCAGTCAGTATGATGAC----- 650  
 QY 147 MetSerPheGlnGluSerLeuGlyAspLeuGlyProPheAspGlnGlySerProPheAla 166  
 DB 649 ---CTGTTCCAGTCCACACACAAATGATGTTCAAGACTGAACAACAGAGCT----- 599  
 QY 167 GlnGluLeuLeuAspAspGlyArgGlnAlaSerProTyTyTyCySerThrTyGlyPro 186  
 DB 598 ---TCATCATGAACACTGTGAAGACNAGAACTATTATATGACCAACTATGCT--- 545  
 QY 187 GlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrProGlnSer 206  
 DB 544 -----AGCACA----- 539  
 QY 207 SerHisAlaSerAspSerGlyGlySerAspValAspLeuAspLeuThrGluSerLysVal 226  
 DB 538 -----GTAGATTGTTGGACAGCAAAACT 515  
 QY 227 PheProArgAspAspPhe-----ThrAspTyLysLysGlyGluProLys 241  
 DB 514 TTTCGCGGCTCAGATCTCCATGACCAACCACTGCTCTCTGTCAGAGTCACCT 455  
 QY 242 HisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGluTyTrpAspCysLeu 261  
 DB 454 GATGTGAAAAAGGCAAGACCCCTCCAAAGTCCACACAAA----- 410  
 QY 262 GluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIleArgAsp 281

DB 409 -----AAGCACAACCCGAGAGGAGCTCTTATGGGAATTCATCCGGAC 365  
 QY 282 IleLeuIleHisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHisGluGly 301  
 DB 364 ATCTCTTGAACCAAGCAAGAACCCAGATTAATAAATGGGAAGCCATCTGAGGCG 305  
 QY 302 ValPheLysPheLeuArgSerGlyAlaValAlaGlnLeuTrpGlyGlnLysLysAsn 321  
 DB 304 GTCTTCAGGTTCTTGAATCAGAGGAGCTGCTCAGCTATGGGGTAAAAAGAAACMAC 245  
 QY 322 SerAspMetThrTyGlyLysLeuSerArgAlaMetArgTyTyTyLysArgGluIle 341  
 DB 244 AGCAGCATGACCTATGAAAGCTCAGCCGAGCTATGATATTAATAAAGGAATTT 185  
 QY 342 LeuGluArgValAspGlyArgArgLeuValTyLysPheGlyLysAsnSerSerGlyTrp 361  
 DB 184 CTGGAGCGCTGTGATGAGCAGAAAGCTGTATATAATTGGGAAGAAATGCCAGAGTGG 125  
 QY 362 LysGluGluGlu 365  
 DB 124 AGAGAAAATGAA 113

RESULT 11  
 US-09-009-913-338  
 Sequence 338, Application US/09009913  
 Patent No. 6087485  
 GENERAL INFORMATION:  
 APPLICANT: Axyx Pharmaceuticals, Inc.  
 TITLE OF INVENTION: Asthma Related Genes  
 NUMBER OF SEQUENCES: 339  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Bozicevic & Reed, LLP  
 STREET: 285 Hamilton Ave, Suite 200  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94301  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/009,913  
 FILING DATE: 21-JAN-1998  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sherwood, Pamela J  
 REGISTRATION NUMBER: 36,677  
 REFERENCE/DOCKET NUMBER: SEQ-4P  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-327-3231  
 TELEFAX: 650-327-3231  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 338:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 848 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: Coding Sequence  
 LOCATION: 1...848  
 OTHER INFORMATION:  
 US-09-009-913-338  
 Alignment Scores:  
 Pred. No.: 4.26e-45 Length: 848  
 Score: 507.00 Matches: 117

Percent Similarity: 52.70% Conservative: 39  
 Best Local Similarity: 39.53% Mismatches: 84  
 Query Match: 25.54% Indels: 56  
 DB: 3 Gaps: 7

US-08-978-217-16 (1-371) x US-09-009-913-338 (1-848)

QY 56 AlasertPrThrSerGluArgProGlnPheTyrSerLysThrGlnValLeuGluTrpIle 75  
 DB 118 AGCCAGTGGAGTGAATACCACTCAGTCTGACCAATACCAAGTGGAGTGGCTG 177  
 QY 76 SerTyrGlnValGlnLysAsnLysTyrAspAlaSerSerIleAspPheSerArgCysAsn 95  
 DB 178 CAGCACTCTCGACCAACCAAGCTAGCTGATGCTCTTCCAGAGTTCGAC 237  
 QY 96 MetAspGlyAlaThrLeuGlySerCysAlaLeuGlnLysValLeuArgLeuValPheGlyPro 115  
 DB 238 ATTACCGGAGAACCTCTGTGACGATGAGTTCGAGGATTACAGAGGCGACAGCTCA 297  
 QY 116 LeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSerAsn-----SerSer 132  
 DB 298 GCTGGGCAAGCTCTCTCAACCACTCAAGTCAAGTGAACGGCCATGACAGT 357  
 QY 133 AspGlnLeuSerTrpIleIleGlnLeuGlnLysAspGlyMetSerPheGlnLysSer 152  
 DB 358 GAC-----CTTTCCAGCTCCGCA 375  
 QY 153 LeuGlyAspLeuGlyProPheAspGlnLysSerProPheAlaGlnLysLeuAspAsp 172  
 DB 376 CACAATGTCATTTGTCAAGCTCAACCAACCACTCT-----TTCATCTGAACACA 426  
 QY 173 GlyArgGlnAlaSerProTyrTyrCysSerThrTyrGlyProGlyAlaProSerProGly 192  
 DB 427 TGGAAAGAAAGAACTATCTATGATCCAGCTATGTAGACAGATGATGATCTGTGAC 486  
 QY 193 SerSerAspValSerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAspSer 212  
 DB 487 AGTAAGACTTTCTGCGCGGCTCAGATCTCCATGACAACTCCAGTCAAC----- 534  
 QY 213 GlyLysSerAspValAspLeuAspLeuThrGlnSerLysValPheProArgAspAspPhe 232  
 DB 535 -----CTTCCAGTTGCAAGTCA----- 552  
 QY 233 ThrAspTyrLysLysGlyGlnProLysHisGlyLysArgLysArgGlyArgProArgLys 252  
 DB 553 CCTGATATGAAAAG---GAGCAAGACCACT----- 582  
 QY 253 LeuSerLysGluTyrTrpAspCysLeuGlnGlyLysLysSerLysHisAlaProArgGly 272  
 DB 583 -----GTAAAGTCCCAACCAAAAGACAAACCAAGAGGC 618  
 QY 273 ThrHisLeuTrpGluPheIleArgAspIleLeuHisProGlnLeuAsnGlnLysLeu 292  
 DB 619 ACTCACTTATGGAGTTCATCCGAGCATTTCTTGAGCCCAAGACAAAGCAAGAGGCTG 678  
 QY 293 MetLysTrpGlnAsnArgHisGlnGlyValPheLysPheLeuArgSerGlnAlaValAla 312  
 DB 679 ATCAATATGGAGAACCTTCCGAGGACATCTCAGGTTCTTAAGTCAGAACTGTGGCT 738  
 QY 313 GlnLeuTrpGlyGlnLysLysLysSerAsnMetThrTyrGlnLysLeuSerArgAla 332  
 DB 739 CAGCTGTGGGAGAAAAGAAATAAAGTACATGACATACGAGAGAGCTCAGCGGCT 798  
 QY 333 MetArgTyrTyrTyrLysArgGlnLysLeuGlnArgValAspGlyArg 348  
 DB 799 ATGAGATATTTACTACAAACGAGAAATCTTGAACTGTGATGACGA 846

RESULT 12  
 US-09-009-913-8  
 ; Sequence 8, Application US/09009913  
 ; Patent No. 6087485  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Axy's Pharmaceuticals, Inc.

;; TITLE OF INVENTION: Asthma Related Genes  
 ;; NUMBER OF SEQUENCES: 339  
 ;; CORRESPONDENCE ADDRESS:  
 ;; ADDRESSEE: Bozicevic & Reed, LLP  
 ;; STREET: 285 Hamilton Ave, Suite 200  
 ;; CITY: Palo Alto  
 ;; STATE: CA  
 ;; COUNTRY: USA  
 ;; ZIP: 94301  
 ;; COMPUTER READABLE FORM:  
 ;; MEDIUM TYPE: Diskette  
 ;; COMPUTER: IBM Compatible  
 ;; OPERATING SYSTEM: DOS  
 ;; SOFTWARE: FastSeq for Windows Version 2.0  
 ;; CURRENT APPLICATION DATA:  
 ;; APPLICATION NUMBER: US/09/009,913  
 ;; FILING DATE: 21-JAN-1998  
 ;; CLASSIFICATION: DATA:  
 ;; PRIOR APPLICATION DATA:  
 ;; APPLICATION NUMBER:  
 ;; FILING DATE:  
 ;; ATTORNEY/AGENT INFORMATION:  
 ;; NAME: Sherwood, Pamela J  
 ;; REGISTRATION NUMBER: 36,677  
 ;; REFERENCE/DOCKET NUMBER: SEQ-4P  
 ;; TELECOMMUNICATION INFORMATION:  
 ;; TELEPHONE: 650-327-3231  
 ;; TELEFAX: 650-327-3231  
 ;; TELEX:  
 ;; INFORMATION FOR SEQ ID NO: 8:  
 ;; SEQUENCE CHARACTERISTICS:  
 ;; LENGTH: 2280 base pairs  
 ;; TYPE: nucleic acid  
 ;; STRANDEDNESS: double  
 ;; TOPOLOGY: linear  
 ;; MOLECULE TYPE: cDNA  
 ;; US-09-009-913-8  
 ;; Alignment Scores:  
 ;; Pred. No.: 8,91e-37 Length: 2280  
 ;; Score: 435.50 Matches: 95  
 ;; Percent Similarity: 46.60% Conservative: 49  
 ;; Best Local Similarity: 30.74% Mismatches: 66  
 ;; Query Match: 21.94% Indels: 99  
 ;; Gaps: 6  
 ;; US-08-978-217-16 (1-371) x US-09-009-913-8 (1-2280)  
 QY 58 TrpThrSerGluArgProGlnPheTyrSerLysThrGlnValLeuGluTrpIleSerTyr 77  
 DB 206 TGGACATCAGTCCACCTCGAATACGTGACTAAGCGCCATGTGTGGAGTGTCTCCAGTTC 265  
 QY 78 GlnValGlnLysAsnLysTyrAspAlaSerSerIleAspPheSerArgCysAsnMetAsp 97  
 DB 266 TCGTCGACACAGTACAACTTGGACACCAATTCATCTCTTGTCACTTCAACTTCACATCTCAGT 325  
 QY 98 GlyAlaThrLeuCysSerCysAlaLeuGlnLysLeuArgLeuValPheGlyProLeuGly 117  
 DB 326 GGCCTGCAGCTGTGTGACATGACACACAGAGAGATTCTTCGAGGACGCTGCGCGC 385  
 QY 118 AspGlnLeuHisAlaGlnLeuArgAspLeuThrSerAsnSerSerAspGlnLeuSerTrp 137  
 DB 386 GAGTACCTGTAC-----TTC 400  
 QY 138 IleIleGlnLeuLeuGlnLysAspGlyMetSerPheGlnLysSerLeuGlyAspLeuGly 157  
 DB 401 ATCTTCAGAACTCCGACACCAAGGTTACTCTTT----- 436  
 QY 158 ProPheAspGlnLysSerProPheAlaGlnLysLeuLeuAspAspGlyArgGlnAlaSer 177  
 DB 437 -----TTTAATGACCGTGAAGAAAGCAAG 460  
 QY 178 ProTyrTyrCysSerThrTyrGlyProGlyAlaProSerProGlySerSerAspValSer 197

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Db 461 -----GCCACCATCAAGACTATGCTGATTCAC 490
Qy 198 ThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAspSerGlySerAspVal 217
Db 491 TGCCTGAAACAAAGTGCATCAAAAGTCAA-----520
Qy 218 AspLeuAspLeuThrGlnSerLysValPheProArgAspAspPheThrAspTyrLysLys 237
Db 520 -----520
Qy 238 GlyGlnProLysHisGlyLysArgGlyArgProArgLysLeuSerLysGluTyr 257
Db 520 -----520
Qy 258 TrpAspCysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGlu 277
Db 521 ----GACTGT-----CACAGTCATAGTAGAACAAAGCTCCAAAGTCTCATCTTATGGGAA 571
Qy 278 PheIleArgAspIleLeuIleHisProGlnLeuAsnGluLysLeuMetLysTrpGluAsn 297
Db 572 TTTGTGAGAACCTGCTTATCTCTGCTGAAAGAAAGCTGGCATTCGGAATGGGAAGAT 631
Qy 298 ArgHisGluGlyValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGln 317
Db 632 AGCGAACAAAGAAATTTTTCGGGTGCTTAAATCCGGAAGCCCTGGCAAGATGCGGGACAA 691
Qy 318 LysLysLysAsnSerAsnMetThrTyrGlnLysLeuSerArgAlaMetArgTyrTyrTyr 337
Db 692 AGGAAGAAATATGACAGAAATGACTATGAAAGTTGAGCAGAGCCCTGAGATGACTATAT 751
Qy 338 LysArgGluIleLeuGluIleArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsn 357
Db 752 AAACACGAAATTTTGAGCCGGGTGAC---CGAAGTTAAGTACAAATTTGGAAAAAT 808
Qy 358 SerSerGlyTyrLysGluGluVal 366
Db 809 GCACACGGGTGCAGAGAACAAAGCTA 835

RESULT 13
US-09-009-913-6
; Sequence 6, Application US/09009913
; Patent No. 6087485
; GENERAL INFORMATION:
; APPLICANT: Axxis Pharmaceuticals, Inc.
; TITLE OF INVENTION: Asthma Related Genes
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,913
; FILING DATE: 21-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: SEQ-4P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3231
; TELEFAX: 650-327-3231

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; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2428 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-009-913-6

Alignment Scores:
Pred. No.: 9,82e-37 Length: 2428
Score: 435.50 Matches: 95
Percent Similarity: 46.60% Conservative: 49
Best Local Similarity: 30.74% Mismatches: 66
Query Match: 21.94% Indels: 99
DB: 3 Gaps: 6

US-08-978-217-16 (1-371) x US-09-009-913-6 (1-2428)
Qy 58 TrpThrSerGluArgProGlnPheTrpSerLysThrGlnValLeuGluTyrPileSerTyr 77
Db 354 TGGACATCAGTCCACCTGTAATCTGACATAAGCCCATGTGTGGAGTGCCTCAAGTTC 413
Qy 78 GlnValGlnLysAsnLysTyrAspAlaSerSerIleAspPheSerArgCysAsnMetAsp 97
Db 414 TGCCTGCACAGTAAAGTTGACACCAATTCATCTCTTGCACCACTTCAACATCAGT 473
Qy 98 GlyAlaThrLeuLysSerGlySalAlaLeuGluIleLeuArgLeuValPheGlyProLeuGly 117
Db 474 GGCTTGACCTGTGTCAGCATAGACACAGAGAGTTGCTGAGGACAGCTGCTTGGGCG 533
Qy 118 AspGlnLeuHisAlaGlnLeuArgAspLeuThrSerAsnSerSerAspGluLeuSerTyr 137
Db 534 GAGTACTCTGAC-----TTC 548
Qy 138 IleIleGlnLeuLeuGluLysAspGlyMetSerPheGlnGlnSerLeuGlyAspLeuGly 157
Db 549 ATCCTCAGAAACATCCGACACACAGAGTTACTCTT-----584
Qy 158 ProPheAspGlnLysSerProPheAlaGlnGlnLeuAspAspArgAlaSer 177
Db 585 -----TTTATAGACCTGAAGAAAGCAAG 608
Qy 178 ProTyrTyrCysSerThrTyrGlyProGlyAlaProSerProGlySerSerAspValSer 197
Db 609 -----GCCACCATCAAAAGACTATGCTGATTCACAC 638
Qy 198 ThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAspSerGlySerAspVal 217
Db 639 TGCCTGAAACAAAGTGCATCAAAAGTCAA-----668
Qy 218 AspLeuAspLeuThrGlnSerLysValPheProArgAspAspPheThrAspTyrLysLys 237
Db 668 -----668
Qy 238 GlyGlnProLysHisGlyLysArgGlyArgProArgLysLeuSerLysGluTyr 257
Db 668 -----668
Qy 258 TrpAspCysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGlu 277
Db 669 ----GACTGT-----CACAGTCATAGTAGAACAAAGCTCCAAAGTCTCATCTTATGGGAA 719
Qy 278 PheIleArgAspIleLeuIleHisProGlnLeuAsnGluLysLeuMetLysTrpGluAsn 297
Db 720 TTTGTAGACAGCTGCTTATCTCTGCTGAAAGAAAGCTGGCATTCGGAATGGGAAGAT 779
Qy 298 ArgHisGluGlyValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGln 317
Db 780 AGGAACAAAGAAATTTTTCGGGTGCTTAAATCCGAGAGCCCTGGCAAGATGCGGGACAA 839
Qy 318 LysLysLysAsnSerAsnMetThrTyrGlnLysLeuSerArgAlaMetArgTyrTyrTyr 337

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Db      840 AGAAGAAAAATGACAGATATGATGAAAAATTGACAGAGCCCTGAGATACTAT 899
      338 LysArgGluIleLeuGluArgValAspGlyArgLeuValTyrLysPheGlyLysAsn 357
      900 AAAACAGAAATTTTGGACCGGTTGAC---CGAAGTTAGTGTACAAATTTGGAAAAAT 956
Qy      358 SerSerGlyTyrLysGluGluGluVal 366
      957 GCACACGGGTGGACAGAGACAGCTA 983

RESULT 14
US-09-009-913-10
; Sequence 10, Application US/09009913
; Patent No. 6087485
; GENERAL INFORMATION:
; APPLICANT: Ays Pharmaceuticals, Inc.
; TITLE OF INVENTION: Asthma Related Genes
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,913
; FILING DATE: 21-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: SEQ-4P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3231
; TELEFAX: 650-327-3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2498 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-009-913-10

Alignment Scores:
Pred. No.: 1,032-36 Length: 2498
Score: 435.50 Matches: 95
Percent Similarity: 46.60% Conservative: 49
Best Local Similarity: 30.74% Mismatches: 66
Query Match: 21.94% Indels: 99
DB: 3 Gaps: 6

US-08-978-217-16 (1-371) x US-09-009-913-10 (1-2498)
Qy      58 TrpThrSerGluArgProGlnPheTyrSerLysThrGlnValLeuGluTyrPheSerTyr 77
      423 TGGACATGATCCACCCCTGATACTGACTAAGCCCATGTGTGGAGTGGCTCCAGTTTC 482
Qy      78 GlnValGluLysAsnLysTyrAspAlaSerSerIleAspPheSerArgCysAsnMetAsp 97
      483 TGCTGGACACAGTACAGTGTGACACCAATGATCTCTTCTGCAACTTCAACATCAGT 542

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Qy      98 GlyAlaThrLeuCysSerCysAlaLeuGluGluLeuArgLeuValPheGlyProLeuGly 117
      543 GGCTGACAGCTGTCCACCATGACACAGAGAGATTCTCGAGGAGCTGCTCGGCG 602
Qy      118 AspGlnLeuHisAlaGlnLeuArgAspLeuThrSerAsnSerSerAspGluLeuSerTyr 137
      603 GAGTACTCTGTAC-----TTC 617
Qy      138 IleIleGluLeuLeuGluLysAspGlyMetSerPheGlnGluSerLeuGlyAspLeuGly 157
      618 ATCTCCAGACATCCGACACAGAGTTACTCTTT----- 653
Qy      158 ProPheAspGlnGlySerProPheAlaGlnGluLeuAspAspGlyArgGlnAlaSer 177
      654 -----TTTAATGACCGCTGAAGAACAG 677
Qy      178 ProTyrTyrCysSerThrTyrGlyProGlyValaProSerProGlySerSerAspValSer 197
      678 -----GCCACATCAAGACTGATGATTTCCAC 707
Qy      198 ThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAspSerGlyGlySerAspVal 217
      708 TGCTTGAACAAACAGTGGCATCAAAAGTCAA----- 737
Qy      218 AspleuAspleuThrGluSerLysValPheProArgAspAspPheThrAspTyrLysLys 237
      737 ----- 737
Qy      238 GlyGluProLysHisGlyLysArgLysArgGlyLysArgGlyLysLeuSerLysGlyTyr 257
      737 ----- 737
Qy      258 TrpAspCysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTyrGlu 277
      738 ---GACTGT-----CACAGTCATAGTAGAACAGCCCTCAAGTTCATCATATGGAA 788
Qy      278 PheIleArgAspIleLeuIleHisPheProGluLeuAsnGluGlyLeuMetLysTyrGluAsn 297
      789 TTTGTACAGACCTGCTTCTATCTCTGAAAGAAACCTGTGCATCTGGAATGGAAAGAT 848
Qy      298 ArgHisGluGlyValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTyrGluGln 317
      849 AGGGAACAGGAATTTTTCGGGTGTTAAATCGAAGCCCTCGCAAGATATGGGACAA 908
Db      909 AGAAGAAAAATGACAGATATGATGAAAAATTGAGCAGAGCCCTGAGATACTAT 968
Qy      318 LysLysLysAsnSerAsnMetThrTyrGluLysLeuSerArgAlaMetArgTyrTyr 337
      909 AGAAGAAAAATGACAGATATGATGAAAAATTGAGCAGAGCCCTGAGATACTAT 968
Qy      338 LysArgGluIleLeuGluArgValAspGlyArgLeuValTyrLysPheGlyLysAsn 357
      969 AAAACAGGAATTTTGGACCGGTTGAC---CGAAGTTAGTGTACAAATTTGGAAAAAT 1025
Qy      358 SerSerGlyTyrLysGluGluGluVal 366
      1026 GCACACGGGTGGACAGAGACAGCTA 1052

RESULT 15
US-08-368-281-1
; Sequence 1, Application US/08368281
; Patent No. 5721113
; GENERAL INFORMATION:
; APPLICANT: Libermann, Towia A
; APPLICANT: Oetgen, Joerg P
; APPLICANT: Kunsch, Charles A
; TITLE OF INVENTION: NERF Genes
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406

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## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/368,281  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk  
REGISTRATION NUMBER: 33,833  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096  
TELEFAX: 610-270-5090  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2975 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-368-281-1

## Alignment Scores:

Pred. No.:	1.69e-15	Length:	2975
Score:	238.50	Matches:	54
Percent Similarity:	52.50%	Conservative:	30
Best Local Similarity:	33.75%	Mismatches:	59
Query Match:	12.02%	Indels:	17
DB:	1	Gaps:	2

US-08-978-217-16 (1-371) x US-08-368-281-1 (1-2975)

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DB 344 GAGGTGTCACTGTAAGAGCTGAACCCATGATACCTCTCTATTCACATCACAGAT 403  
QY 215 SerAspValAspLeuAspLeuThrGlnSerLysValPheProArgAspAspPheThrAsp 234  
DB 404 AGCCATGAACCAATGAAAAAGAAAGTTGGCCGTAAACCAAGAACCAATCACCA 463  
QY 235 TyrLysLysGlyLysProLysHisGlyLysArgLysArgGlyArgProArgLysLeuSer 254  
DB 464 ATTCCAATGGGTCTCTGAGTATGATTAAGAAACCAAGA----- 508  
QY 255 LysGluTyrTrpAspCysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHis 274  
DB 509 -----GAAGGAAAAAGAAACACA-----ACCTAT 532  
QY 275 LeuTrpGluPheIleArgAspIleLeuIleHisProGluLeuAsnGluGlyLeuMetLys 294  
DB 533 TTGTGGAGTTCTTTAGATCTACTCAAGATTAATAAATCTGTCCACGATATTATAA 592  
QY 295 TrpGluAsnArgHisGluGlyValPheLysPheLeuArgSerGluAlaValAlaGlnLeu 314  
DB 593 TGGACTCAGAGAGAAAAGCATATTCAAGCTGTGATTCAAAGCTGTCTTAAGCTT 652  
QY 315 TyrGlyGlnLysLysLysAsnSerAsnMetThrTyrGluLysLeuSerArgAlaMetArg 334  
DB 653 TGGGGAAGCATGAACAACCAACGACATGATAAACAATGAGGAGCTTTGAGA 712  
QY 335 TyrTyrTyrLysArgGluIleLeuGluArgValAspGlyArgArgLeuValTyrLysPhe 354  
DB 713 TACTACTACCAAGAGGAGATTTTGCAAGGTGAAGACAGAGGCTTGATATCAAGTTC 772

Search completed: March 15, 2003, 23:33:28  
Job time : 93.0238 secs

